PAGE: 1

## RAW SEQUENCE LISTING PATENT APPLICATION US/08/575,361

Teen 7#5

DATE: 06/07/96 TIME: 09:43:18

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1 2	SEQUENCE LISTING  Corrected Diskette Needeline	
3 4	(1) GENERAL INFORMATION:	ed
5 6	(i) APPLICANT: Chandrasegaran, Srinivasan	
7 8 9	(ii) TITLE OF INVENTION: A GENERAL METHOD TO CLONE HYBRID RESTRICTION ENDONUCLEASES USING lig GENE	
10 11	(iii) NUMBER OF SEQUENCES: 35	
12 13 14 15	<ul><li>(iv) CORRESPONDENCE ADDRESS:</li><li>(A) ADDRESSEE: Cushman Darby &amp; Cushman L.L.P.</li><li>(B) STREET: 1100 New York Avenue, NW, Ninth Floor, East Tower</li></ul>	
16 17 18 19 20	(C) CITY: Washington (D) STATE: DC (E) COUNTRY: USA (F) ZIP: 20005-3918	
21 22 23 24 25 26	<pre>(v) COMPUTER READABLE FORM:     (A) MEDIUM TYPE: Floppy disk     (B) COMPUTER: IBM PC compatible     (C) OPERATING SYSTEM: PC-DOS/MS-DOS     (D) SOFTWARE: PatentIn Release #1.0, Version #1.25</pre>	
27 28 29 30 31	(B) COMPUTER: 1BM PC compatible  (C) OPERATING SYSTEM: PC-DOS/MS-DOS  (D) SOFTWARE: Patentin Release #1.0, Version #1.25  (vi) CURRENT APPLICATION DATA:  (A) APPLICATION NUMBER: US/08/575,361  (B) FILING DATE: 20-DEC-1995  (C) CLASSIFICATION: 435  (viii) ATTORNEY/AGENT INFORMATION:  (A) NAME: Kokulis, Paul N.  (B) REGISTRATION NUMBER: 16,773	H
32 33 34 35 36	(viii) ATTORNEY/AGENT INFORMATION:  (A) NAME: Kokulis, Paul N.  (B) REGISTRATION NUMBER: 16,773  (C) REFERENCE/DOCKET NUMBER: PNK/4130/213779/DJP	
37 38 39 40 41	(ix) TELECOMMUNICATION INFORMATION:  (A) TELEPHONE: 202-861-3000  (B) TELEFAX: 202-822-0944  (C) TELEX: 6714627 CUSH	
42 43 44	(2) INFORMATION FOR SEQ ID NO:1:	
45 46 47 48	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 23 amino acids  (B) TYPE: amino acid  (D) TOPOLOGY: linear	

Explanation of error that occurred throughout the Sequence Listing:

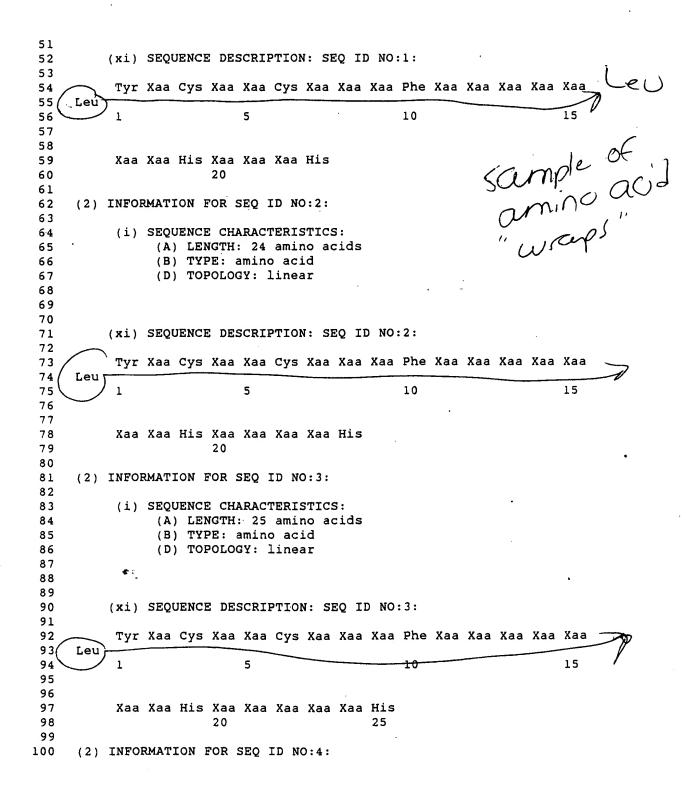
For all of your nucleic acid and amino acid sequences, the text at the end of each line "wrapped" down to the next line. This occurred if your file was retrieved in a word processor after creating it in PatentIn. Your word processor probably has different margin settings than those used in PatentIn. (A right margin set at least to .3 in your word processor will prevent wrapping). Please submit your original ".app" file that can be found in the /patentin/projects subdirectory.

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## RAW SEQUENCE LISTING PATENT APPLICATION US/08/575,361

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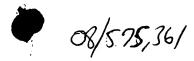
## RAW SEQUENCE LISTING PATENT APPLICATION US/08/575,361

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(2) INFORMATION FOR SEQ ID NO:23:	emple of
A LA CERCUENCE CUARACTERIZA	1012 alid
(1) SEQUENCE CHARACTERISTICS:	10,10
(A) DENGIN: /4 Dase pairs /	2 0 l
(B) TIPE: NUCLEIC acid	$\alpha \beta s$ .
(C) STRANDEDNESS: SINGLE	<b>'</b>
(D) TOPOLOGI: Tinear	
•	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:	
CUCGACCAAA CCHAGGHICG AAGGGCCCCH HCHHAAGCHC CHCCGAGAG	ec liccageligaa
	J.
GGACAUCUCC AUGG _ ] ( )	
/ - / - / T	
(2) INFORMATION FOR SEQ ID NO:24:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 87 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	·
(D) TOPOLOGY: linear	
•	
(X1) SEQUENCE DESCRIPTION: SEQ ID NO:24:	<i>( ( ( ( ( ( ( ( ( (</i>
CONTRANCE TENERCONTES COCTOS CON CONCEDENCE CNECCOCO	TO CHOCHOTACH 60
/ 6	3G GIGGICIAGI
00	
ATCGTTCAAT GATACTTCAT GGAATTC	
87)	
(2) INFORMATION FOR SEQ ID NO:25:	
	•
(i) SEQUENCE CHARACTERISTICS:	•
(A) LENGTH: 23 base pairs	
(B) TYPE: nucleic acid	S 41 -
(b) TIPE: Nucleic acid	Entire
(C) STRANDEDNESS: single	Entire
(C) STRANDEDNESS: single	Entire 1:stmg
(C) STRANDEDNESS: single	1:5+12
(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(C) STRANDEDNESS: single	1:stmq
(C) STRANDEDNESS: single (D) TOPOLOGY: linear  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:	1:5+12
(C) STRANDEDNESS: single (D) TOPOLOGY: linear  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:  CCCCTGAAGG AGATATACAT ATG	not shown.
(C) STRANDEDNESS: single (D) TOPOLOGY: linear  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:	not shown.
(C) STRANDEDNESS: single (D) TOPOLOGY: linear  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:  CCCCTGAAGG AGATATACAT ATG	not shown.
(C) STRANDEDNESS: single (D) TOPOLOGY: linear  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:  CCCCTGAAGG AGATATACAT ATG	not shown.
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•	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 74 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:  CUCGACCAAA CCUAGGUUCG AAGGGCCCCU UCUUAAGCUC CUCCGAGAC  (60)  GGACAUCUCC AUGG (74)  (2) INFORMATION FOR SEQ ID NO:24:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 87 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:  GGATECAAGC TTAGCGATCT GCCTGCAGGT CGACTCTAGC CAGGGGCGC  (60)  ATCGTTCAAT GATACTTCAT GGAATTC  (2) INFORMATION FOR SEQ ID NO:25:  (i) SEQUENCE CHARACTERISTICS:



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For Further Information Contact: Meredith Beckhardt at 703-308-421